

J. Li



1600

RAW SEQUENCE LISTING

DATE: 02/11/2002

PATENT APPLICATION: US/09/602,833A

TIME: 09:50:45

Input Set : A:\8535036999.txt

Output Set: N:\CRF3\02112002\I602833A.raw

ENTERED

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4 <110> APPLICANT: Turner, Alex
5     Zambrowicz, Brian
6     Nehls, Michael
7     Freidrich, Glenn A.
8     Sands, Arthur T.
10 <120> TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
11     ENCODED THEREBY
13 <130> FILE REFERENCE: 8535-0036-999
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/602,833A
C--> 15 <141> CURRENT FILING DATE: 2000-06-23
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1116
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapien
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)...(1113)
28 <400> SEQUENCE: 1
29   atg gga cat aaa gtg gtt gtc ttc gac att tct gtc atc aga gcc ttg      48
30   Met Gly His Lys Val Val Val Phe Asp Ile Ser Val Ile Arg Ala Leu
31   1           5           10          15
33   tgg gaa act cgt gtc aag aag cac aaa gct tgg cag aag aag gag gtg      96
34   Trp Glu Thr Arg Val Lys Lys His Lys Ala Trp Gln Lys Lys Glu Val
35   20          25          30
37   gaa agg ctt gag aag agc gcc ttg gag aag ata aag gag gag tgg aac      144
38   Glu Arg Leu Glu Lys Ser Ala Leu Glu Lys Ile Lys Glu Glu Trp Asn
39   35          40          45
41   ttt gtg gcc gaa tgc agg agg aag ggc atc ccc cag gct gta tac tgc      192
42   Phe Val Ala Glu Cys Arg Arg Lys Gly Ile Pro Gln Ala Val Tyr Cys
43   50          55          60
45   aag aat ggc ttc ata gac acc agc gtg cgg ctt ctg gac aag att gaa      240
46   Lys Asn Gly Phe Ile Asp Thr Ser Val Arg Leu Leu Asp Lys Ile Glu
47   65          70          75          80
49   agg aac act ctc aca agg cag agt tca ctt ccc aag gac aga ggc aaa      288
50   Arg Asn Thr Leu Thr Arg Gln Ser Ser Leu Pro Lys Asp Arg Gly Lys
51   85          90          95
53   cgg agc agt gcg ttt gtg ttt gaa ctt tct ggg gag cac tgg acg gag      336
54   Arg Ser Ser Ala Phe Val Phe Glu Leu Ser Gly Glu His Trp Thr Glu
55   100         105         110
57   ctc cca gat tca ttg aag gag cag aca cac ctg aga gaa tgg tac ata      384
58   Leu Pro Asp Ser Leu Lys Glu Gln Thr His Leu Arg Glu Trp Tyr Ile

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59	115	120	125	
61	agc aat acc ttg att caa atc att cct aca tat att cag tta ttt caa	432		
62	Ser Asn Thr Leu Ile Gln Ile Ile Pro Thr Tyr Ile Gln Leu Phe Gln			
63	130	135	140	
65	gcg atg aga att ctg gat ctg cca aaa aac caa atc tca cat ctt cca	480		
66	Ala Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro			
67	145	150	155	160
69	gca gaa atc ggt tgt ttg aag aac ctg aaa gaa ctc aat gtg ggt ttc	528		
70	Ala Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe			
71	165	170	175	
73	aac tat ctg aag agc att cct cca gaa ttg gga gat tgt gaa aat cta	576		
74	Asn Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu			
75	180	185	190	
77	gag aga ctg gat tgt tct gga aat cta gaa tta atg gag ctg ccc ttt	624		
78	Glu Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe			
79	195	200	205	
81	gaa tta agt aat ttg aag caa gtt aca ttt gta gat atc tca gca aac	672		
82	Glu Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn			
83	210	215	220	
85	aag ttt tcc agt gtc cca atc tgt gtc ctg cgg atg tgc aat ttg cag	720		
86	Lys Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln			
87	225	230	235	240
89	tgg ttg gat atc agc agc aat aac ctg acc gac ctg ccg caa gat ata	768		
90	Trp Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile			
91	245	250	255	
93	gac agg cta gag gag ctg cag agc ttt ctc ttg tat aaa aac aag ttg	816		
94	Asp Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu			
95	260	265	270	
97	acc tac ctt ccc tat tcc atg ctg aac ctg aag aag ctc act ctg tta	864		
98	Thr Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu			
99	275	280	285	
101	gtc gtc agt ggg gac cat ttg gtg gag ctc cca act gcc ctt tgt gac	912		
102	Val Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp			
103	290	295	300	
105	tca tcc aca cct tta aaa ttt gta agc ctt atg gac aat cct att gat	960		
106	Ser Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp			
107	305	310	315	320
109	aat gcc caa tgt gaa gat ggc aat gaa ata atg gaa agt gaa cgg gat	1008		
110	Asn Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp			
111	325	330	335	
113	cgc caa cat ttt gat aaa gaa gtt atg aaa gcc tat att gaa gac ctt	1056		
114	Arg Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu			
115	340	345	350	
117	aaa gaa aga gaa tct gtt ccc agc tat acc acc aaa gtg tct ttt agc	1104		
118	Lys Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser			
119	355	360	365	
121	ctt caa ctt tga	1116		
122	Leu Gln Leu			
123	370			

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126 <210> SEQ ID NO: 2
127 <211> LENGTH: 371
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapien
131 <400> SEQUENCE: 2
132 Met Gly His Lys Val Val Val Phe Asp Ile Ser Val Ile Arg Ala Leu
133   1           5           10           15
134 Trp Glu Thr Arg Val Lys Lys His Lys Ala Trp Gln Lys Lys Glu Val
135           20           25           30
136 Glu Arg Leu Glu Lys Ser Ala Leu Glu Lys Ile Lys Glu Glu Trp Asn
137           35           40           45
138 Phe Val Ala Glu Cys Arg Arg Lys Gly Ile Pro Gln Ala Val Tyr Cys
139           50           55           60
140 Lys Asn Gly Phe Ile Asp Thr Ser Val Arg Leu Asp Lys Ile Glu
141           65           70           75           80
142 Arg Asn Thr Leu Thr Arg Gln Ser Ser Leu Pro Lys Asp Arg Gly Lys
143           85           90           95
144 Arg Ser Ser Ala Phe Val Phe Glu Leu Ser Gly Glu His Trp Thr Glu
145           100          105          110
146 Leu Pro Asp Ser Leu Lys Glu Gln Thr His Leu Arg Glu Trp Tyr Ile
147           115          120          125
148 Ser Asn Thr Leu Ile Gln Ile Ile Pro Thr Tyr Ile Gln Leu Phe Gln
149           130          135          140
150 Ala Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro
151           145          150          155          160
152 Ala Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe
153           165          170          175
154 Asn Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu
155           180          185          190
156 Glu Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe
157           195          200          205
158 Glu Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn
159           210          215          220
160 Lys Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln
161           225          230          235          240
162 Trp Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile
163           245          250          255
164 Asp Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu
165           260          265          270
166 Thr Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu
167           275          280          285
168 Val Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp
169           290          295          300
170 Ser Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp
171           305          310          315          320
172 Asn Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp
173           325          330          335
174 Arg Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu
175           340          345          350

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176 Lys Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser
177          355          360          365
178 Leu Gln Leu
179      370
181 <210> SEQ ID NO: 3
182 <211> LENGTH: 681
183 <212> TYPE: DNA
184 <213> ORGANISM: Homo sapien
186 <220> FEATURE:
187 <221> NAME/KEY: CDS
188 <222> LOCATION: (1)...(678)
190 <400> SEQUENCE: 3
191 atg aga att ctg gat ctg cca aaa aac caa atc tca cat ctt cca gca      48
192 Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro Ala
193   1          5          10          15
195 gaa atc ggt tgt ttg aag aac ctg aaa gaa ctc aat gtg ggt ttc aac      96
196 Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe Asn
197   20          25          30
199 tat ctg aag agc att cct cca gaa ttg gga gat tgt gaa aat cta gag      144
200 Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu Glu
201   35          40          45
203 aga ctg gat tgt tct gga aat cta gaa tta atg gag ctg ccc ttt gaa      192
204 Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe Glu
205   50          55          60
207 tta agt aat ttg aag caa gtt aca ttt gta gat atc tca gca aac aag      240
208 Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn Lys
209   65          70          75          80
211 ttt tcc agt gtc cca atc tgt gtc ctg cgg atg tcg aat ttg cag tgg      288
212 Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln Trp
213   85          90          95
215 ttg gat atc agc agc aat aac ctg acc gac ctg ccg caa gat ata gac      336
216 Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile Asp
217  100          105          110
219 agg cta gag gag ctg cag agc ttt ctc ttg tat aaa aac aag ttg acc      384
220 Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu Thr
221  115          120          125
223 tac ctt ccc tat tcc atg ctg aac ctg aag aag ctc act ctg tta gtc      432
224 Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu Val
225  130          135          140
227 gtc agt ggg gac cat ttg gtg gag ctc cca act gcc ctt tgt gac tca      480
228 Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser
229  145          150          155          160
231 tcc aca cct tta aaa ttt gta agc ctt atg gac aat cct att gat aat      528
232 Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn
233   165          170          175
235 gcc caa tgt gaa gat ggc aat gaa ata atg gaa agt gaa cgg gat cgc      576
236 Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp Arg
237   180          185          190
239 caa cat ttt gat aaa gaa gtt atg aaa gcc tat att gaa gac ctt aaa      624

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```

240  Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu Lys
241      195                      200                      205
243  gaa aga gaa tct gtt ccc agc tat acc acc aaa gtg tct ttt agc ctt      672
244  Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser Leu
245      210                      215                      220
247  caa ctt tga
248  Gln Leu
249  225
252 <210> SEQ ID NO: 4
253 <211> LENGTH: 226
254 <212> TYPE: PRT
255 <213> ORGANISM: Homo sapien
257 <400> SEQUENCE: 4
258  Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro Ala
259      1          5          10          15
260  Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe Asn
261      20          25          30
262  Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu Glu
263      35          40          45
264  Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe Glu
265      50          55          60
266  Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn Lys
267      65          70          75          80
268  Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln Trp
269      85          90          95
270  Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile Asp
271      100         105         110
272  Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu Thr
273      115         120         125
274  Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu Val
275      130         135         140
276  Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser
277      145         150         155         160
278  Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn
279      165         170         175
280  Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp Arg
281      180         185         190
282  Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu Lys
283      195         200         205
284  Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser Leu
285      210         215         220
286  Gln Leu
287  225

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VERIFICATION SUMMARY

DATE: 02/11/2002

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TIME: 09:50:46

Input Set : A:\8535036999.txt

Output Set: N:\CRF3\02112002\I602833A.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date